

AMENDMENTS TO THE CLAIMS:

The following is the status of the claims of the above-captioned application, as amended.

Claims 1-18 (Canceled.)

18. (Previously presented.) A cyclomaltodextrin glucanotransferase variant having an amino acid sequence which differs from the amino acid sequence of a parent cyclomaltodextrin glucanotransferase, wherein the parent cyclomaltodextrin glucanotransferase is a *Bacillus* cyclomaltodextrin glucanotransferase and the difference between the amino acid sequence of the cyclomaltodextrin glucanotransferase variant and the amino acid sequence of the parent cyclomaltodextrin glucanotransferase comprises one or more of the following:

47C; 47D; 47E; 47F; 47G; 47I; 47K; 47N; 47P; 47S; 47T; 47V; 47W; 47Y;
145D; 145H; 145I; 145N; 145Q; 145V;
146H; 146L; 146T; 146V; 146Y;
147C; 147E; 147N; 147Q;
196C; 196E; 196F; 196H; 196I; 196K; 196M; 196P; 196Q; 196R; 196T; 196V; 196W;
196Y; and

371C; 371F; 371H; 371K; 371M; 371R; 371T; 371W;

wherein each position corresponds to the position of the amino acid sequence of the mature Cyclomaltodextrin glucanotransferase obtained from *Bacillus circulans* strain 251.

19. (Previously presented.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the parent cyclomaltodextrin glucanotransferase is cyclomaltodextrin glucanotransferase is derived from a *Bacillus* selected from the group consisting of *Bacillus autolyticus*, *Bacillus cereus*, *Bacillus circulans*, *Bacillus circulans* var. *alkalophilus*, *Bacillus coagulans*, *Bacillus firmus*, a strain of *Bacillus halophilus*, *Bacillus macerans*, *Bacillus megaterium*, *Bacillus ohbensis*, *Bacillus stearothermophilus*, *Bacillus subtilis*.

20. (Previously presented.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the parent cyclomaltodextrin glucanotransferase is derived from a strain of *Bacillus circulans* or a mutant or a variant thereof.

21. (Previously presented.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the parent cyclomaltodextrin glucanotransferase is derived from a strain of *Bacillus stearothermophilus*.

22. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises 47C; 47D; 47E; 47F; 47G; 47I; 47K; 47N; 47P; 47S; 47T; 47V; 47W; or 47Y.
23. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises 145D; 145H; 145I; 145N; 145Q; or 145V.
24. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises 146H, 146L; 146T; 146V; or 146Y.
25. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises 147C; 147E; 147N; or 147Q.
26. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises 196C; 196E; 196F; 196H; 196I; 196K; 196M; 196P; 196Q; 196R; 196T; 196V; 196W; or 196Y.
27. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises 196H.
28. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises 371C; 371F; 371H; 371K; 371M; 371R; 371T; or 371W.
29. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises D371R.
30. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises:
- 47K/145E/146V/147N;
 - 47K/145E/146E/147N;
 - 47K/145D/146R/147D;
 - 47K/145D/146E/147D;
 - 47K/145E/146V/147N/196H;

47K/145E/146E/147N/196H;
47K/145E/146V/147N/196H/371R;
47K/145E/146E/147N/196H/371R;
47K/145D/146R/147D/196H;
47K/145D/146E/147D/196H;
47K/145D/146R/147D/196H/371R;
47K/145D/146R/147D/196H/371R;
47K/196H;
47R/196H;
145E/146V/147N;
145E/146E/147N;
145D/146R/147D;
145D/146E/147D;
47K/371R; or
47R/371R.

31. (Currently amended.) The cyclomaltodextrin glucanotransferase variant of claim 18, wherein the difference in amino acid positions comprises:

S145E/E146V/T147N;
S145E/T147N;
S145D/E146R/T147D;
S145D/T147D;
S145E/E146V/T147N/D196H;
S145E/T147N/D196H;
S145E/E146V/T147N/D196H/D371R;
S145E/T147N/D196H/D371R;
S145D/E146R/T147D/D196H;
S145D/T147D/D196H;
S145D/E146R/T147D/D196H/D371R;
S145D/E146R/T147D/D196H/D371R;
S145E/E146V/T147N;
S145E/T147N;
S145D/E146R/T147D;
S145D/T147D;
K47R/D371R; or
K47R/D196H.

32. (Previously presented.) A method of producing a cyclodextrin, comprising treating a starch with a cyclomaltodextrin glucanotransferase variant of claim 18.
33. (Previously presented.) The method of claim 32, wherein the cyclodextrin is a α -cyclodextrin.
34. (Previously presented.) The method of claim 32, wherein the cyclodextrin is a β -cyclodextrin.
35. (Previously presented.) The method of claim 32, wherein the cyclodextrin is a γ -cyclodextrin.